

SEQUENCE LISTING

<110> Sagami Chemical Research Center

5 <120> Human Proteins Having Transmembrane Domains and DNAs Encoding these Proteins

<130> 660857

<140>

<141>

10

<150> Japan 9-323129

<151> 1997-11-25

<160> 12

15

<170> Windows 95 (Word 98)

 $\langle 210 \rangle$ 1

<211> 269

20

<212> PRT

<213> Homo sapiens

<400> 1

Met Gly Gln Asn Asp Leu Met Gly Thr Ala Glu Asp Phe Ala Asp Gln

25

1 5 10 15

Phe Leu Arg Val Thr Lys Gln Tyr Leu Pro His Val Ala Arg Leu Cys

20 25 30

35 40 45

50 55 60

65 70 75 80

85 90 95

10 100 105 110

115 120 125

130 135 140

145 150 155 160

165 170 175

20 180 185 190

195 200 205

210 215 220

225 230 235 240

Gln Thr Met Ser Val Ile Gly Gly Leu Leu Leu Val Val Ala Leu Gly

5 <210> 2
 <211> 311
 <212> PRT
 <213> Homo sapiens

10 <400> 2

Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro Leu

1 5 10 15

Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu

20 25 30

15 Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly

35 40 45

His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro

50 55 60

Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val

20 65 70 75 80

Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His

85 90 95

Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile

100 105 110

25 Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala

115 120 125

Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe

Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg

Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly

Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile

Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe

10 Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys

Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val

Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu

Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val

Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly

20 Ala Leu Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe Thr Phe Val Leu

Gln Leu Met Gly Asp Arg Asn

25 $\langle 210 \rangle_3$

<211> 383

<212> PRT

$\langle 400 \rangle$ 3

5 1 5 10 15

20 25 30

35 40 45

50 55 60

65 70 75 80

15 85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

25 165 170 175

180 185 190

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp

195 200 205

Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val

210 215 220

5 Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp

225 230 235 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His

245 250 255

Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu

10 260 265 270

Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly

275 280 285

Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu

290 295 300

15 Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val

305 310 315 320

Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile

325 330 335

Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro

20 340 345 350

Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln

355 360 365

Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly

370 375 380

25

<210> 4

<211> 807

001260-2261560

<212> DNA

<213> Homo sapiens

<400> 4

5 atgggccaga acgacctgat gggcacggcc gaggacttcg ccgaccagtt cctccgtgtc 60
 acaaagcagt acctgcccc a cgtggcgcg cctctgtctga tcagcacctt cctggaggac 120
 ggcatccgta tgtggtcca gtggagcgag cagcgcgact acatcgacac cacctggaac 180
 tgcggctacc tgctggcctc gtccttcgtc ttctcaact tgctgggaca gctgactggc 240
 tgcgtcctgg tgttgagcag gaacttcgtg cagtacgcct gcttcgggct ctttggaatc 300
 10 atagctctgc agacgattgc ctacagcatt ttatgggact tgaagtttt gatgaggaac 360
 ctggccctgg gaggaggcct gttgctgctc ctacgagaat cccgttctga agggaagagc 420
 atgtttcgcg gcgtccccac catgcgtgag agctccccc aacagtacat gcagctcgga 480
 ggcagggtct tgctggttct gatgttcac accctcctc actttgacgc cagcttctt 540
 tctattgtcc agaacatcgt gggcacagct ctgatgatt tagtggccat tggttttaa 600
 15 accaagctgg ctgctttgac tcttgtgtg tggctctttg ccatcaacgt atattcaac 660
 gccttctgga ccatccagt ctacaagccc atgcatgact tctgaaata cgacttctc 720
 cagaccatgt cggtgattgg gggcttgctc ctggtggtgg ccctgggccc tgggggtgtc 780
 tccatggatg agaagaagaa ggagtgg 807

20 <210> 5

<211> 933

<212> DNA

<213> Homo sapiens

25 <400> 5

atgtccaacc ccagcgcccc accaccatat gaagaccgca accccctgta cccaggccct 60
 ctgccccctg ggggctatgg gcagccatct gtctgccag gagggatatcc tgcctaccct 120

ggctaccgc agcctggcta cggtcaccct gctggctacc cacagccat gccccacc 180
 caccgatgc ccatgaacta cggcccaggc catggctatg atggggagga gagagcggg 240
 agtgatagct tcgggcttgg agagtgggat gaccggaaag tgcgacacac tttatccga 300
 aaggtttact ccatcatctc cgtgcagctg ctcatcactg tggccatcat tgctatcttc 360
 5 acctttgtgg aacctgtcag cgcctttgtg aggagaaatg tggctgtcta ctacgtgtcc 420
 tatgtgtctc tcgtgtcac ctacgtgatc ctgacctgt gccagggacc cagacgcgt 480
 ttccatgga acatcattct gctgaccctt ttacttttg ccatgggctt catgacgggc 540
 accatttcca gtatgtacca aaccaaagcc gtcacattg caatgatcat cactgcgggtg 600
 gtatccattt cagtcacat ctctgcttt cagaccaagg tggacttcac ctctgtcaca 660
 10 ggctcttct gtgtcttggg aattgtgtc ctggtgactg ggattgtcac tagcattgtg 720
 ctctacttcc aatacgttta ctggtccac atgctctatg ctgcttggg ggccattgt 780
 ttcacctgt tctggctta cgacacacag ctggtcctgg ggaaccggaa gcacaccatc 840
 agccccgagg actacatcac tggcgccctg cagatttaca cagacatcat ctacatcttc 900
 acctttgtgc tgcagctgat gggggatcgc aat 933

15

<210> 6
 <211> 1149
 <212> DNA
 <213> Homo sapiens

20

<400> 6
 atggcaggga ttccagggt cctcttctt ctcttcttc tgctctgtgc tgttgggcaa 60
 gtgagccctt acagtcccc ctggaaacce acttggcctg cataccgct cctgtctgc 120
 ttgccccagt ctacctcaa tttagccaag ccagacttg gagccgaagc caaattagaa 180
 25 gtatcttctt catgtggacc ccagtgtcat aagggaactc cactgcccac ttacgaagag 240
 gccaaagcaat atctgtctta tgaaacgtc tatgccaatg gcagccgcac agagacgcag 300
 gtgggcatct acatctcag cagtagtgga gatggggccc aacaccgaga ctcagggtct 360

00423-03400

5

15

20

25

ctg atg ggc acg gcc gag gac ttc gcc gac cag ttc ctc cgt gtc aca 163
Leu Met Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr

Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg Val Leu Leu

170 175 180
 att gtc cag aac atc gtg ggc aca gct ctg atg att tta gtg gcc att 691
 Ile Val Gln Asn Ile Val Gly Thr Ala Leu Met Ile Leu Val Ala Ile
 185 190 195
 ggt ttt aaa acc aag ctg gct gct ttg act ctt gtt gtg tgg ctc ttt 739
 Gly Phe Lys Thr Lys Leu Ala Ala Leu Thr Leu Val Val Trp Leu Phe

	250	255	260	
20	atg gat gag aag aag aag gag tgg taa cagtcacaga tccctacctg			930
	Met Asp Glu Lys Lys Lys Glu Trp			

265
cctggctaag acccgtggcc gtcaaggact ggttcggggt ggattcaaca aaactgccag 990
cttttatgta tcctcttccc tccccctccc ttggtaaagg cacagatgtt ttgagaactt 1050
25 tatttcaga gacacctgag aatcgatggc tcagtctgct ctggagccac agtctggcgt 1110
ctgacccttc agtgcaggcc agcctggcag ctggaagcct cccccacgcc gaggccttgg 1170
agtgaacagc ccgcttggct gtggcatctc agtctctatt ttgagttttt ttgtgggggt 1230

acaggagggg gccttcaagc tgtactgtga gcagacgcac ttgtattatc attcaaagca 1290
gtctccctct tatttgtaag ttacatttt tagcggaac tactaaatta tttgggtgg 1350
ttcagccaaa cctcaaaaca gttaatctcc ctggtttaa atcacaccag tggctttgat 1410
gtgtttctg ccccgcatg tttttatag gaatactgaa aacatttagg gacacccaaa 1470
5 gaatgatgca gtattaaagg ggtggtagaa gctgctgtt atgataaaag tcacgggtca 1530
gaaatcagc ttggattggt gccaaagtgt ttattgggta acaccctggg agtttagta 1590
gcttgaggca aggtggaggg gcaagaagtc ctgggggaag ctgctggtct ggggtctgct 1650
ggctccaag ctggcagtg gaagggctag tgagaccaca caggggtagc cccagcagca 1710
gcaccctgca agccagcctg gccagctgct cagaccagct tcagagccg cagccgctgt 1770
10 gggcaggggg tgtggcagga gctccagca ctggagacc acggactca cccagttacc 1830
tcacatgggg cttttctga gcaaggtct gaaagcgcag gccgcctgg ctgagcagca 1890
ccgcccttc ccagctgcac tcgccctgtg gacagcccc acacaccact ttctgagggc 1950
tgtcgtcac tcagattgtc cgttgctat gccgaatgca gccaaaattc cttttacaa 2010
tttgtgatgc ctaccgatt tgatctaat cctgtattta aagtttcta acactgcctt 2070
15 atactgtgtt tctcttttg ggggagctta actgctgtt gctccctgct gtctgcacca 2130
tagtaaagtc cacaagggtg gtcgaacacc tctctggccc ctgacctat ctggggacag 2190
gctggctcag cctgtctcca gggctgtgc ggcccagccc cgagcctgcc tccctctgg 2250
cctctcatcc attggctctg cagggcaggg gtgaggcagg ttctgtctca taagtgttt 2310
tggaagtcac ctacctttt aacacagccg aactagtccc aacgcgttg caaatattcc 2370
20 cctggtagcc tacttctta cccccgaata ttgtaagat cgatcaatgg ctcaggaca 2430
tgggttctct tctctgtga tcattcaagt gctcactgca tgaagactgg cttgtctcag 2490
tgtttcaacc tcaccagggc tgtctcttg tccacacctc gctccctgtt agtgccgtat 2550
gacagcccc atcaaatgac ctggccaag tcacggttc tctgtgtca aggttggtg 2610
gctgattggt ggaaagtagg gtggacaaa ggaggccacg tgagcagtc gcaccagttc 2670
25 tgcaccagca gcgcctcct cctagtgggt gttctgttt ctctggccc tgggtgggt 2730
agggcctgat tcgggaagat gccttgcag ggaggggagg ataagtggga tctaccaatt 2790
gattctggca aaacaattc taagatttt ttgctttatg tgggaaacag atctaaatct 2850

cattttatgc tgtattttat atcttagttg tgtttgaaaa cgttttgatt tttggaaaca 2910

catcaaaaata aataatggcg tttgttgt 2938

<210> 8

5 <211> 269

<212> PRT

<213> Homo sapiens

<400> 8

10

Met Gly Gln Asn Asp

1 5

Leu Met Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr

10 15 20

Lys Gln Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile Ser Thr Phe

15

25 30 35

Leu Glu Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu Gln Arg Asp

40 45 50

Tyr Ile Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala Ser Ser Phe

55 60 65

20

Val Phe Leu Asn Leu Leu Gly Gln Leu Thr Gly Cys Val Leu Val Leu

70 75 80 85

Ser Arg Asn Phe Val Gln Tyr Ala Cys Phe Gly Leu Phe Gly Ile Ile

90 95 100

Ala Leu Gln Thr Ile Ala Tyr Ser Ile Leu Trp Asp Leu Lys Phe Leu

25

105 110 115

Met Arg Asn Leu Ala Leu Gly Gly Gly Leu Leu Leu Leu Ala Glu

120 125 130

007220.2209500

1 5 10

Asp Arg Asn Pro Leu Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly

cag cca tct gtc ctg cca gga ggg tat cct gcc tac cct ggc tac ccg 209

30 35 40

10 Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro

acc cac ccg atg ccc atg aac tac ggc cca ggc cat ggc tat gat ggg 305

60 65 70 75

Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp

cgg aaa gtg cga cac act ttt atc cga aag gtt tac tcc atc atc tcc 401

20 95 100 105

Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val

gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct gtc tac tac gtg 497

125 130 135

tcc tat get gtc ttc gtt gtc acc tac ctg atc ctt gcc tgc tgc cag 545

140 145 150 155

Gly Pro Arg Arg Arg Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe

5 160 165 170

Thr Phe Ala Met Gly Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln

175 180 185

acc aaa gcc gtc atc att gca atg atc atc act gcg gtg gta tcc att 689

10 Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile

190 195 200

tca gtc acc atc ttc tgc ttt cag acc aag gtg gac ttc acc tcg tgc 737

Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys

205 210 215

15 aca ggc ctc ttc tgt gtc ctg gga att gtg ctc ctg gtg act ggg att 785

Thr Gly Leu Phe Cys Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile

220 225 230 235

gtc act agc att gtg ctc tac ttc caa tac gtt tac tgg ctc cac atg 833

Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met

20 240 245 250

ctc tat gct gct ctg ggg gcc att tgt ttc acc ctg ttc ctg gct tac 881

Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr

255 260 265

gac aca cag ctg gtc ctg ggg aac cgg aag cac acc atc agc ccc gag 929

25 Asp Thr Gln Leu Val Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu

270 275 280

gac tac atc act ggc gcc ctg cag att tac aca gac atc atc tac atc 977

Phe Thr Phe Val Leu Gln Leu Met Gly Asp Arg Asn

5 300 305 310

caagccccc tttcacccg atcctgggct ctccctcca agctagaggg ctgggcccta 1080
tgactgtggt ctgggcttta ggcccccttc ctcccccttg agtaacatgc ccagtttctt 1140
ttctgtcctg gagacagggt gcctctctgg ctatggatgt gtgggtactt ggtggggacg 1200
gaggagctag ggactaactg ttgctcttgg tgggcttggc agggactagg ctgaagatgt 1260
gtcttctccc cgccacctac tgtatgacac cacattcttc ctaacagctg gggttgtgag 1320
gaatatgaaa agagcctatt cgatagctag aagggaatat gaaaggtaga agtgacttca 1380
aggtcacgag gtccccctcc cacctctgtc acaggcttct tgactacgta gttggagcta 1440
tttttcccc cagcaaagcc agagagcttt gtccccggcc tcttgacac ataggccatt 1500
atcctgtatt cctttggctt ggcatctttt agctcaggaa ggtagaagag atctgtgccc 1560
atgggtctcc ttgcttcaat ccttcttctt ttacgtgaca tatgtattgt ttatctgggt 1620
tagggatggg ggacagataa tagaacgagc aaagtaacct atacaggcca gcatggaaca 1680
gcatctcccc tgggcttgct cctggcttgt gacgtataa gacagagcag gccacatgtg 1740
gccatctgct cccattctt gaaagctgct ggggcctcct tgcaggcttc tggatctctg 1800
gtcagagtga actcttgctt cctgtattca ggcagctcag agcagaaagt aaggggcaga 1860
gtcatacgtg tggccaggaa gtagccaggg tgaagagaga ctcggtgcgg gcaggggaaa 1920
tgcctggggg tccctacct ggctagggag ataccgaagc ctactgtggt actgaagact 1980
tctgggttct ttcttctgc taaccagggt agggctctaa gaggaagggt acttctctct 2040
gtttgtctta agttgactg ggggatttct gacttgaggc ccattctctc agccagccac 2100
tgccttcttt gtaatatata gtgccttgag ctggaatggg gaagggggac aagggtcagt 2160
ctgtcgggtg ggggcagaaa tcaaatcagc ccaaggatat agttaggatt aattacttaa 2220
tagagaaatc ctaactatat cacacaaagg gatacaacta taaatgtaat aaaatttatg 2280
tctagaagtt

2290

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu

5 1 5 10 15

10 **Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn**

15 tca tgt gga ccc cag tgt cat aag gga act cca ctg ccc act tac gaa 360
 Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu
 65 70 75

cgc aca gag acg cag gtg ggc atc tac atc ctc agc agt agt gga gat 456
 Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp
 100 105 110

cgg cag att tat ggc tat gac agc agg ttc agc att ttt ggg aag gac 552

130 135 140

Phe Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly

tgc acc ggc acc ctg gtg gca gag aag cat gtc ctc aca gct gcc cac 648

160 165 170 175

10 Cys Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg

gtg ggc ttc cta aag ccc aag ttt aaa gat ggt ggt cga ggg gcc aac 744

195 200 205

Asp Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg

gtg aaa cgc acc cat gtg ccc aag ggt tgg atc aag ggc aat gcc aat 840

20 225 230 235

Asp Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro

cac aag aga aaa ttt atg aag att ggg gtg agc cct cct gct aag cag 936

260 265 270

ctg cca ggg ggc aga att cac ttc tct ggt tat gac aat gac cga cca 984

275 280 285

Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp

ttg ctc tac cag caa tgc gat gcc cag cca ggg gcc agc ggg tct ggg 1080

305 310 315

10 Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys

att att ggc att ttt tca ggg cac cag tgg gtg gac atg aat ggt tcc 1176

340 345 350

Pro Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala

cag att tgc tat tgg att aaa gga aac tac ctg gat tgt agg gag ggg 1272

20 370 375 380

ggccaaattg tttttgtca ttggcgtgca cacgtgtgtg tgtgtgtgtg tgtgtaaggt 1390

actggtttgt gtatcatatc atatatcatt taagcagttt gaaggcatac ttttgcatag 1510

cgtttttgca aactttgatt ttatttcat ctgaacttgt ttcaaagatt tatattaaat 1630

attggcata caagagatat gaattcttat atgtgtgcat gtgtgttttc ttctgagatt 1690

catcttggtg gtgggttttt ttgtttttt aattcagtc ctgatctta atgcttccat 1750
aaggcagtgt tcccatttag gaactttgac agcatttggt aggcagaata ttttgattt 1810
ggaggcattt gcatggtagt ctttgaacag taaaatgatg tgttgactat actgatacac 1870
atattaaact ataccttata gtaaaccagt atcccaagct gcttttagtt ccaaaaatag 1930
5 tttcttttcc aaaggttggt gctctacttt gtaggaagtc ttgcatatg gccctcccaa 1990
ctttaaagtc ataccagagt ggccaagagt gtttatccca acccttccat ttaacaggat 2050
ttcactcaca ttctggaac tagctatttt tcagaagaca ataatcaggg ctttaattaga 2110
acaggctgta ttctctccca gcaaacagtt gtggccacac taaaaacaat catagcattt 2170
tacccttgga ttatagcaca tctcatgttt tatcatttgg atggagtaat ttaaaatgaa 2230
10 ttaaattcca gagaacaatg gaagcattgc ctggcagatg tcacaacaga ataaccactt 2290
gtttggagcc tggcacagtc ctccagcctg atcaaaaatt attctgcata gtttccagt 2350
tgctttctgg gagctatgta cttcttcaat ttggaaactt ttctctctca ttatagtga 2410
aaatacttgg aagtacttt aagaaaacca gtgtggcctt ttccctcta gctttaaag 2470
ggccgctttt gctggaatgc tctaggttat agataaaca ttaggtataa tagcaaaaat 2530
15 gaaaattgga agaatgcaaa atggatcaga atcatgcctt ccaataaagg cctttacaca 2590
tgttttatca atatgattat caaatcacag catatacaga aaagacttgg acttattgta 2650
tgtttttatt ttatggctct cggcctaage acttcttctt aatgtatcg gagaaaaaat 2710
caaatggact acaagcacgt gtttgctgtg cttgcacccc aggtaaacct gcattgtagc 2770
aatttgaag gatattcaga tggagcactg tcaacttagac attctctggg ggattttctg 2830
20 cttgtcttc ttgagctttt tggaaggata attctgataa ggcactcaag aaacgtacaa 2890
ccacagtgtc ttcttcaa atcatgagaa atactatgca tagcaaggag atgcagagcc 2950
gccaggaaaa ttctgagttc cagcacaatt ttctttggaa tctaacagga atctagcctg 3010
aggaagaagg gaggtctcca ttctatgtc tggattttgg gggttttgtt tgttttgct 3070
ttagcttggg gaaaaaaagt tcaactgaaca ccaagaccag aatggatttt ttaaaaaaaa 3130
25 tagatgttcc ttttgtgaag caccttgatt ccttgatttt gattttttgc aaagttagac 3190
aatggcacia agtcaaaatg aaatcaatgt ttagttcaca agtagatgta atttactaaa 3250
gaatgataca cccatagtct atatacagct taactcacag aactgtaaaa gaaaattata 3310

aaataattca acatgtccat ctttttagtg ataataaaag aaagcatggt attaaactat 3370
 catagaagta gacagaaaaa gaaaaaagga ctcatggcat tattaatata attagtgcctt 3430
 tacatgtgtt agttatacat attagaagca tatttgcta gtaaggctag tagaaccaca 3490
 ttcccaaag tgtgctcctt aaacactcat gccttatgat ttctaccaa aagtaaaaag 3550
 5 ggttgattta agtcagagga agatgcctct ccattttccc tctctttatc agagggtcac 3610
 atgcctgtct gcacattaaa agctctggga agacctgttg taaagggaca agttgaggtt 3670
 gtaaaatctg catttaata aacatctttg atcac 3705

<210> 12

10 <211> 383

<212> PRT

<213> Homo sapiens

<400> 12

15 Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu

1 5 10 15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr

20 25 30

Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn

20 35 40 45

Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser

50 55 60

Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu

65 70 75

25 Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser

80 85 90 95

Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp

001230 001230 001230

100 105 110
 Gly Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys
 115 120 125
 Arg Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp
 5 130 135 140
 Phe Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly
 145 150 155
 Cys Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His
 160 165 170 175
 10 Cys Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg
 180 185 190
 Val Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn
 195 200 205
 Asp Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg
 15 210 215 220
 Val Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn
 225 230 235
 Asp Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 240 245 250 255
 20 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln
 260 265 270
 Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro
 275 280 285
 Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp
 25 290 295 300
 Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly
 305 310 315

10